

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/815,773DATE: 04/30/97  
TIME: 14:54:29

INPUT SET: S17329.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: Baumgartner, James W.  
Farrah, Theresa M.  
Foster, Donald C.  
Grant, Frank J.  
O'Hara, Patrick J.

(ii) TITLE OF INVENTION: Testis-Specific Receptor

(iii) NUMBER OF SEQUENCES: 33

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.  
(B) STREET: 1201 Eastlake Avenue East  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98102

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E.  
(B) REGISTRATION NUMBER: 31,648  
(C) REFERENCE/DOCKET NUMBER: 95-33

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206-442-6673  
(B) TELEFAX: 206-442-6678

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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47      (A) LENGTH: 1289 base pairs
48      (B) TYPE: nucleic acid
49      (C) STRANDEDNESS: double
50      (D) TOPOLOGY: linear
51
52      (ii) MOLECULE TYPE: cDNA
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 49..1191
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      CCCCCCGCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC      57
63                                     Met Ala Phe
64                                     1
65
66      GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA      105
67      Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr
68          5              10              15
69
70      TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT      153
71      Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro
72          20              25              30              35
73
74      CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG      201
75      Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu
76          40              45              50
77
78      CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG      249
79      Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val
80          55              60              65
81
82      GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC      297
83      Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr
84          70              75              80
85
86      ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG      345
87      Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys
88          85              90              95
89
90      GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT      393
91      Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn
92      100              105              110              115
93
94      GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA      441
95      Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser
96          120              125              130
97
98      CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT      489
99      Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr

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	135	140	145	
100				
101				
102	TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA			537
103	Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val			
104	150	155	160	
105				
106	CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT			585
107	Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp			
108	165	170	175	
109				
110	CAT GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA			633
111	His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile			
112	180	185	190	195
113				
114	GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT			681
115	Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr			
116	200	205	210	
117				
118	ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT			729
119	Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr			
120	215	220	225	
121				
122	TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT			777
123	Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr			
124	230	235	240	
125				
126	CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC			825
127	Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser			
128	245	250	255	
129				
130	ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG			873
131	Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu			
132	260	265	270	275
133				
134				
135	ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA			921
136	Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu			
137	280	285	290	
138				
139	ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA			969
140	Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val			
141	295	300	305	
142				
143	GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT			1017
144	Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser			
145	310	315	320	
146				
147	GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA			1065
148	Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys			
149	325	330	335	
150				
151	ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT			1113
152	Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val			

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153      340              345              350              355
154
155  ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA      1161
156  Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys
157              360              365              370
158
159  ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT CCATATCAAG      1208
160  Met Ile Pro Glu Phe Phe Cys Asp Thr
161              375              380
162
163  AGACATGGTA TTGACTCAAC AGTTTCCAGT CATGGCCAAA TGTTCATAT GAGTCTCAAT      1268
164
165  AACTGAATT TTTCTTGCGA A      1289
166
167
168  (2) INFORMATION FOR SEQ ID NO:2:
169
170      (i) SEQUENCE CHARACTERISTICS:
171          (A) LENGTH: 380 amino acids
172          (B) TYPE: amino acid
173          (D) TOPOLOGY: linear
174
175      (ii) MOLECULE TYPE: protein
176
177      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
178
179
180  Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
181      1              5              10              15
182
183  Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
184              20              25              30
185
186  Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
187              35              40              45
188
189  Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
190              50              55              60
191
192  Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
193      65              70              75              80
194
195  Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
196              85              90              95
197
198  Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
199              100              105              110
200
201  Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
202              115              120              125
203
204  Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
205      130              135              140

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206
207 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
208 145 150 155 160
209
210 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
211 165 170 175
212
213 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
214 180 185 190
215
216 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
217 195 200 205
218
219 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
220 210 215 220
221
222 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
223 225 230 235 240
224
225 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
226 245 250 255
227
228 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
229 260 265 270
230
231 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
232 275 280 285
233
234 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
235 290 295 300
236
237 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
238 305 310 315 320
239
240 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
241 325 330 335
242
243 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
244 340 345 350
245
246 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
247 355 360 365
248
249 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
250 370 375 380
251
252

```

## (2) INFORMATION FOR SEQ ID NO:3:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1167 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/815,773**

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Line

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Original Text